Claims:

1. A recombination process for recombining a population of heterologous polynucleotides comprising variant groups and/or regions, wherein recombination is performed within one group of polynucleotides and/or between defined regions of polynucleotides by using different restriction sites in different groups and/or regions of polynucleotides.

2. A recombination process according to claim 1,
   - wherein the polynucleotides comprise at least one section defining a structural unit and at least one section defining an interstructural motif;
   - wherein in the population at least two variant interstructural motifs are present;
   - wherein variant interstructural motifs are recombined separately by using different restriction sites in different interstructural motifs.

3. A recombination process for recombining at least two polynucleotides comprising at least a structural unit and at least one interstructural motif, comprising
   - cleaving the polynucleotides with at least one restriction enzyme creating a non-palindromic cohesive end thus creating a recombination site;
   - wherein the recombination site is present in the interstructural motif which comprises a coding region of the polynucleotide;
   - ligating the resulting mixture of fragments.

4. A recombination process according to at least one of the above claims, characterised in that polynucleotides are recombined wherein the structural unit of different polynucleotides are heterologous and wherein

the structural units are optionally made of structural subunits which are connected by interstructural motifs.

5. A recombination process according to claim 3, wherein the structural units and/or the structural subunits are recombined.

6. A recombination process according to claim 2, 3 or 4, wherein the interstructural motif comprises a coding region of the polynucleotide, a non-coding region or a part of a vector sequence.

7. A recombination process according to at least one of the above claims , wherein at least one restriction enzyme is used which creates a non-palindromic cohesive end.

8. A recombination process according to at least one of the above claims, wherein the restriction endonuclease creating the non-palindromic cohesive end is a PRE.

9. A recombination process according to at least one of the above claims, wherein polynucleotides are recombined which are present in a vector.

10. A recombination process according to at least one of the above claims,
- wherein the polynucleotides are cleaved with at least one restriction enzyme creating non-palindromic cohesive ends,
- wherein the cleaved vectors are ligated at high DNA concentrations allowing the formation of concatemers,
- wherein the concatemers are resolved by cleavage with at least one further restriction enzyme
- wherein the vector constructs are recircularised by ligation.

11. A recombination process according to at least one of the above claims, wherein for different interstructural motifs different restriction enzymes are used thus creating unique sites for recombination.

12. A recombination process according to at least one of the above claims, wherein for different interstructural motifs the same restriction enzymes is used wherein the nucleotides are different at the cleavage site in different interstructural motifs thus creating unique restriction sites for recombination.

13. A recombination process according to at least one of the above claims, wherein a resolving enzyme is used which creates cohesive ends.

14. A recombination process according to at least one of the above claims, wherein a resolving enzyme is used which creates non-palindromic cohesive ends.

15. A recombination process according to at least one of the above claims, wherein the restriction site for the resolving enzyme is present in the interstructural motif.

16. A recombination process according to at least one of the above claims, wherein the binding sites for one or more restriction enzymes and/or the nucleotide variation at the cleavage site are introduced by site specific mutation at predefined positions.

17. A recombination process according to at least one of the above claims, wherein the polynucleotides are vector constructs comprising sequence sections defining at least two structural units.

18. A recombination process according to at least one of the above claims, wherein the polynucleotides comprise a variant gene family.

19. A recombination process according to at least one of the above claims,
    - wherein the polynucleotides comprise a section encoding at least a variable heavy fragment of an antibody and/or a section encoding at least a variable light fragment of an antibody.

20. A recombination process according to at least one of the above claims, wherein a population of polynucleotides is recombined wherein the polynucleotides encode at least the variable fragment of an antibody which defines the structural unit,
wherein the CDR regions of the variable fragment define the structural subunits that are recombined with each other and at least the FRs define the interstructural motifs,
wherein at least two different subclasses of the variable fragments are encoded by the polynucleotide population thus defining different groups,
wherein recombination is performed within each subclass separately by using for each subclass a different restriction site in the interstructural motif.

21. A process according to at least one of the above claims, wherein the variable heavy fragment comprises the VH and CH1 domains and the and variable light fragments comprise the VL and the CL domains.

22. A process according to at least one of the above claims, wherein the different framework subclasses present in the population of polynucleotides which are recombined are cleaved with different restriction enzymes creating cohesive ends.

23. A process according to at least one of the above claims, wherein the restriction site is present within the FR3.

24. A process according to at least one of the above claims, wherein the polynucleotides encode the variable heavy and the variable light fragment of an antibody.

25. A process according to at least one of the above claims, wherein at least one additional recombination site is located between the variable heavy and the variable light fragment which is used for shuffling the variable heavy fragment against the variable light fragment.

26. A process according to at least one of the above claims, wherein a restriction endonuclease is used for shuffling the variable heavy fragment against the variable light fragment, which creates non-palindromic cohesive ends.

27. A process according to at least one of the above claims, wherein the polynucleotides are vector constructs which comprise sections encoding the variable heavy and the variable light fragment of an antibody, wherein at least two different subclasses of the variable fragments (heavy and/or light fragment) are encoded by the polynucleotide population thus defining different groups,

- wherein the vectors are cleaved with at least one restriction enzyme creating a non-palindromic cohesive end at a restriction site present in-between the sections encoding the variable heavy and the variable light fragment of an antibody thus allowing recombination between the heavy and the light fragments;
- wherein upon usage of the at least one restriction enzyme a different cohesive end site is created in each group;
- wherein the fragments are ligated thus allowing the formation of concatemers containing only members of one group;
- wherein the concatemers are resolved by the use of at least one restriction enzyme at a restriction site present at an interstructural motif.

28. A process wherein, for resolving of the concatemers different restriction enzymes are used for different subclasses.

29. A process according to at least one of the above claims, wherein a phage and/or phagemid display vector is used as a vector.

30. A method for evolving a molecule by selection and recombination comprising a recombination process according to at least one of the above claims.

31. The method according to claim 30 comprising:
    a.) creating a starting library by cloning the polynucleotides to be recombined into an expression vector if the polynucleotide itself is not a vector
    b.) recombining the library members with a process according to at least one of the above claims 1 to 29
    c.) selecting candidates with desired characteristics
    d.) optionally performing further rounds of selection and recombination.

32. The method according to at least one of the above claims, wherein the library members respective the selected candidates are recombined with themselves or with other selected clones or members of the naive library.

33. The method according to at least one of the above claims, wherein the polynucleotides are expressed via a method which allows physical coupling of pheno- and genotype.

34. The method according to at least one of the above claims, wherein the recombined polynucleotides are expressed in a cell and selection is performed by screening or selecting for a particular phenotype amongst the clones.

35. The method according to at least one of the above claims, wherein the oligonucleotides are selected for physical properties.

36. The method according to at least one of the above claims, wherein a display library is created.

37. The method according to at least one of the above claims, wherein the selection step comprises selection for affinity to a defined target.

38. The method according to at least one of the above claims, wherein a phagemid library is created.

39. The method according to at least one of the above claims, wherein the polynucleotides are mutagenised.

40. The method according to at least one of the above claims, wherein further recombination processes are performed in addition to the recombination processes according to at least one of the above claims.

41. The method according to at least one of the above claims, wherein the further recombination processes are in vitro and/or in vivo recombination processes.

42. The method according to at least one of the above claims 31 to 41, wherein after step a.) and before step b.) a selection procedure is.

43. The method according to at least one of the above claims, wherein recombination is performed at a type IIs restriction site already present in the library.

44. A library containing heterologous polynucleotides comprising variant groups and/or variant regions within the polynucleotide, wherein the members of one group and/or the same regions have identical unique restriction sites which differ from the restriction sites present in other groups and/or regions.

45. A library according to claim 44, wherein the polynucleotides comprise at least one section defining a structural unit and at least one section defining an interstructural motif, wherein in the population at least two variant interstructural motifs are present.

46 A library according to claim 44 or 45, wherein the structural unit of different polynucleotides are heterologous and wherein the structural units are optionally made of structural subunits connected by interstructural motifs.

47 A library according to at least one of the above claims wherein the polynucleotides are or are present in a vector.

48. A library according to at least one of the above claims, wherein the interstructural motif comprises a coding region of the polynucleotide, a non-coding region or part of the vector sequence.

49. A library according to at least one of the above claims, wherein the unique restriction sites are located at the interstructural motifs.

50. A library according to at least one of the above claims, wherein at least one interstructural motif has a binding site for a PRE.

51. A library according to at least one of the above claims, wherein the polynucleotides are derived from nature and/or are at least partially synthetical polynucleotides sequences.

52. A library according to at least one of the above claims, wherein the polynucleotides comprise a variant gene family.

53. A library according to at least one of the above claims,
- wherein the polynucleotides comprise a section encoding at least a variable heavy fragment of an antibody and/or a section encoding at least a variable light fragment of an antibody.

54. A library according to at least one of the above claims,
wherein the polynucleotides encode at least the variable fragment of an antibody which defines the structural unit,
wherein the CDR regions of the variable fragment define the structural subunits and at least the FRs define the interstructural motifs,
wherein at least two different subclasses of the variable fragments are encoded by the polynucleotide population thus defining different groups, wherein each subclass has a different restriction site in the interstructural motif.

55. A library according to at least one of the above claims, wherein the variable heavy fragment comprises the VH and CH1 domains and the and variable light fragments comprise the VL and the CL domains.

56. A library according to at least one of the above claims, wherein the restriction site for a resolving enzyme is present within the FR3 of the heavy chain.

57. A library according to on of the above claims, wherin the restriction site for a resolving enzyme is present within the FR3 the light chain.

58. A library according to at least one of the above claims, wherein the polynucleotides encode the variable heavy and the variable light fragment of an antibody.

59. A library according to at least one of the above claims, wherein at least one additional recombination site is located between the variable heavy and the variable light fragment which is used for shuffling the variable heavy fragment against the variable light fragment.

60. A library according to at least one of the above claims, wherein the polynucleotides are vector constructs which comprise sections encoding at least the variable heavy and the variable light fragment of an antibody, wherein at least two different subclasses of the variable fragments (heavy and/or light fragment) are encoded by the polynucleotide population thus defining different groups.

61. A library according to at least one of the above claims, wherein the vector is a phage or phagemid vector.

62. A process for producing a substance with special characteristics, comprising
- recombining and selecting a polynucleotide library for special characteristics according to at least one of the claims 44 to 60 according to a process according to claim 1 to 43,
- recovering at least one clone comprising the polynucleotide depicting the desired characteristic,
  amplifying said polynucleotide in vivo or in vitro
- manufacturing the substance which is either the expression product of the polynucleotide or comprises the latter.

63. Use of a molecule generated from a library according to claim 61 by a method or process according to at least one of the above claims for the treatment of diseases or for therapy.

64. Use of the products derived by the process of the present invention for deriving human therapeutic antibodies and antibody fragment conjugates.

65. Use of antibodies or antibody fragments generated from sequences which are selected from a library according to at least one of the above claims according to method or process according to at least one of the above claims, as diagnostics and/or therapeutic products for the treatment of diseases including immune dysregulation (including psoriasis), cancer, septic and toxic shock, blood haemostasis, nerve regeneration, pain, psychological disorders, appetite dysregulation, sexual dysfunction and wound healing or for vaccines.

66. Use of antibodies or antibody fragments generated from sequences which are selected from a library according to at least one of the above claims according to method or process according to at least one of the above claims for targeted delivery of pharmaceuticals to differentiated or neoplastic animal or human cells or as cosmeceutical.